

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:24:57 ; Search time 76.45 Seconds
(without alignments)
174,239 Million cell updates/sec

Title: US-09-351-778a-11

Sequence: 1 MTSSTAPPTDYKNTATGCL.....LICCLKRRRAPSLLLOYD 77

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.protist:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriophage:*
17: sp.archaeoprotein:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	83.1	101	12	Q91023
2	48	62.3	101	12	Q91276
3	18	23.4	94	12	Q12392
4	7	9.1	83	12	Q88422
5	7	9.1	87	10	Q94H62
6	7	9.1	102	11	Q9D126
7	7	9.1	160	16	Q96268
8	7	9.1	160	16	Q92XL7
9	7	9.1	197	16	Q9JSG7
10	7	9.1	207	4	Q96DJ9
11	7	9.1	228	2	Q9RAX8
12	7	9.1	245	8	Q9T3Y9
13	7	9.1	249	12	Q92466
14	7	9.1	309	5	Q95WFS
15	7	9.1	316	10	Q9C926
16	7	9.1	387	16	Q99X15

17	7	9.1	391	16	Q97GC3	Q97GC3 clostridium
18	7	9.1	392	10	Q9AX94	Q9AX94 oryza sativ
19	7	9.1	404	5	Q9VIM7	Q9VIM7 drosophila
20	7	9.1	476	10	Q9LIP4	Q9LIP4 oryza sativ
21	7	9.1	490	10	Q9FSS8	Q9FSS8 oryza sativ
22	7	9.1	536	5	Q45994	Q45994 caenorhabditis
23	7	9.1	635	5	Q9VJ77	Q9VJ77 drosophila
24	7	9.1	649	5	Q9NKP0	Q9NKP0 drosophila
25	7	9.1	965	2	Q92494	Q92494 bacteroides
26	7	9.1	1175	16	Q91356	Q91356 pseudomonas
27	7	9.1	1401	11	Q9JKD4	Q9JKD4 mus musculus
28	7	9.1	1847	5	Q9NKN5	Q9NKN5 leishmania
29	7	9.1	2499	5	Q9N9N0	Q9N9N0 leishmania
30	6	7.8	26	4	Q9N9B3	Q9N9B3 homo sapien
31	6	7.8	53	8	Q78735	Q78735 flammulina
32	6	7.8	53	13	Q9VH36	Q9VH36 coturnix co
33	6	7.8	64	2	Q9F347	Q9F347 streptomyces
34	6	7.8	69	13	Q9DEC6	Q9DEC6 gallus galli
35	6	7.8	73	13	Q87603	Q87603 chimpanzee
36	6	7.8	76	4	Q96EN4	Q96EN4 homo sapien
37	6	7.8	77	12	Q64888	Q64888 avian adeno
38	6	7.8	79	12	Q9PX71	Q9PX71 human herpe
39	6	7.8	83	16	Q9PEU4	Q9PEU4 xylella fas
40	6	7.8	89	10	Q94T51	Q94T51 oryza sativ
41	6	7.8	89	16	Q9A887	Q9A887 caulobacter
42	6	7.8	91	4	Q9H4V4	Q9H4V4 homo sapien
43	6	7.8	92	2	Q93SB6	Q93SB6 frankia sp.
44	6	7.8	94	16	Q9PCB2	Q9PCB2 xylella fas
45	6	7.8	94	16	Q9PCAS	Q9PCAS xylella fas

ALIGNMENTS

RESULT 1
ID Q91023 PRELIMINARY: PRT: 101 AA.
AC Q91023;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 11.6K PROTEIN.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
CN NCBI_TaxId=10515;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=105;
RA "Adenoviruses of subgenus C with different organ tropism."
RL Submitted (Sep-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ293915; CAC67721.1; -
SQ SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 83.1%; Score 64; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.8e-60;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 APTTDRNTATGTSALNLPQVAFVNDASLDMMFSTALMFVCLIMLICKLR 66
DB 7 APTTDRNTATGTSALNLPQVAFVNDASLDMMFSTALMFVCLIMLICKLR 66
QY 67 ARPP 70
DB 67 ARPP 70
RESULT 2
ID Q91276 PRELIMINARY: PRT: 101 AA.
AC Q91276;
DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE 11.6K PROTEIN.
 OS Human adenovirus type 2.
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 NC NCB1_TaxID=10515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PREI;
 RA Borchering F., Ping-Akerblom P.;
 RT "Adenoviruses of subgenus c with different organ tropism";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A2793913; CAC67704.1; -;
 SO SEQUENCE 101 AA; 11704 MW; E13857DC5891B85B CRC64;

Query Match 62.3%; Score 48; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 4.2e-43;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ALNLPVHAFVNDMSLDMMFSLMFLVCLIMLVCCLCKRRRAPP 70
 DB 23 ALNLPVHAFVNDMSLDMMFSLMFLVCLIMLVCCLCKRRRAPP 70

RESULT 3
 ID 012392 PRELIMINARY; PRT: 94 AA.
 AC 012392;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-JAN-1998 (Tremblrel. 05, Last annotation update)
 DE 11.6K PROTEIN.
 GN AD1/E3-11.6K.
 OS Human adenovirus type 1.
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 NC NCB1_TaxID=10533;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HANOVER / ADRIAN;
 RA Reichmann H., Scharschmidt E., Geisler B., Hausmann J., Ortmann D.,
 RA Bauer U., Flunker G., Seidel W.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11257; CAA72127.1; -;
 DR EMBL: Y11032; CAA71916.1; -;
 SO SEQUENCE 94 AA; 10674 MW; D11485AFE771862 CRC64;

Query Match 23.4%; Score 18; DB 12; Length 94;
 Best Local Similarity 100.0%; Pred. No. 2.3e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 41 MMFSLMFLVCLIML 58
 DB 35 MMFSLMFLVCLIML 52

RESULT 4
 ID 088422 PRELIMINARY; PRT: 83 AA.
 AC 088422;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SPV1-C74, COMPLETE GENOME.
 OS Spiroplasma virus.
 CC Viruses; unclassified viruses.
 NC NCB1_TaxID=12338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Bebear C.M., Aulio P., Bove J., Renaudin J.;
 RT "Spiroplasma citri virus spv1. Characterization of viral sequences

RT present in the spiroplasma host chromosome."
 RL Curr. Microbiol. 32:1-7(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Renaudin J.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U28974; AAA85015.1; -;
 SO SEQUENCE 83 AA; 9398 MW; D4969373B02BFFA8 CRC64;

Query Match 9.1%; Score 7; DB 12; Length 83;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSAL 24
 DB 30 TGLTSAL 36

RESULT 5
 ID 094H62 PRELIMINARY; PRT: 87 AA.
 AC 094H62;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 9.9 KDA PROTEIN.
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Ehrhartoideae; Oryzaceae; Oryza.
 NC NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
 RA Brenner M., Burgess S., Hance M., Shwartsbeyn M., Tsitrin T.,
 RA Riggs F., Hsiao J., Zisman V., Blunt S., Pal G., Vanaken S.E.,
 RA Uterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSNBNB0057P1 genomic sequence."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084767; AAK72273.1; -;
 KW Hypothetical protein.
 SO SEQUENCE 87 AA; 9941 MW; 092E2A6E9D0A42CE CRC64;

Query Match 9.1%; Score 7; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LKRRAR 68
 DB 48 LKRRAR 54

RESULT 6
 ID 09D126 PRELIMINARY; PRT: 102 AA.
 AC 09D126;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE A930014B1IRIK PROTEIN.
 GN A930014B1IRIK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=RETINA;

RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guenrich S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK020853; BAB3222.1; -;
 DR MGI: MGI:1924349; A930014B11RLK.
 SO SEQUENCE 102 AA; 11333 MW; 173C4E191A1477DB CRC64;

Query Match 9.1%; Score 7; DB 11; Length 102;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 RPSLL 74
 Db 86 RPSLL 92

RESULT 7
 O98268 PRELIMINARY; PRT; 160 AA.
 AC O98268;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE MUR9079 PROTEIN.
 GN MUR9079.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Phyllobacteriaceae; Mesorhizobium.
 CX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MAF303099;
 RA MEDLINE-21082930; PubMed-11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Matanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 KW EMBL: AP003015; BAB54491.1; -;
 KM Plasmid: Complete proteome.
 SO SEQUENCE 160 AA; 17656 MW; 85A9C5A9233D9A50 CRC64;

Query Match 9.1%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 Db 28 TGSTIAP 34

RESULT 8
 O92XL7 PRELIMINARY; PRT; 160 AA.
 AC O92XL7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL PROTEIN SMA2279.
 GN SMA2279.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSymb (megaplasmid 1).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.
 CX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1021;
 RX MEDLINE-21396509; PubMed-11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barnet-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Barjau M., Hong A., Huizar L., Hyman R.W., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymb megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AE007307; AAK65885.1; -;
 KW Hypothetical protein; Plasmid; Complete proteome.
 SO SEQUENCE 160 AA; 17966 MW; 9BABAEBE18A1BE34 CRC64;

Query Match 9.1%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 Db 28 TGSTIAP 34

RESULT 9
 O9JSG7 PRELIMINARY; PRT; 197 AA.
 AC O9JSG7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CT142 HYPOTHETICAL PROTEIN_2.
 GN CT142.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 CX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J138;
 RA MEDLINE-20330349; PubMed-10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CW1029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR EMBL: AP002545; BAA98469.1; -;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000531; TonB_box.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN.1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC.1; UNKNOWN.1.
 SO SEQUENCE 197 AA; 22016 MW; EAA69A27851F790D CRC64;

Query Match 9.1%; Score 7; DB 16; Length 197;
 Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGTTSA 23
|||||||

DB 74 ATGTTSA 80

RESULT 10

O96DJ9 PRELIMINARY; PRT: 207 AA.

AC O96DJ9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE CNA FLJ25310 FIS, CLONE SYN00991.
OS Homo sapiens (Human).
DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-STNOVIAL MEMBRANE (KNEE);
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Houta T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.,
*NEBO human cDNA sequencing project."
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK58039; BAB71635.1; -
SQ SEQUENCE 207 AA; 22532 MW; 8E8A17008E924F0 CRC64;

Query Match 9.1%; Score 7; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 RPSLL 74
|||||||

DB 68 RPSLL 74

RESULT 11

O9RBX8 PRELIMINARY; PRT: 228 AA.

AC O9RBX8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 24.1 KDA PROTEIN.
OS Pseudomonas indologera.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Vogesella*.
OX NCBI_TaxId=45465;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC19706;
RA van de Loo F.J., Keese P., Llewellyn D.;
*Structural and regulatory genes controlling indigoldine production in
RT *Vogesella indologera*: involvement of a peptide synthetase homolog."
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
DR EMBL; AF088856; AAD54003.1; -
DR InterPro: IPR001647; HTH_Tetr.
DR Pfam: PF00440; tetr.1
DR PRINTS; PR00455; HTHTR.
KW DNA-binding; Hypothetical protein; Transcription regulation.
SQ SEQUENCE 228 AA; 24140 MW; A928D14F404859B CRC64;

Query Match 9.1%; Score 7; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 22;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 64 RRRARP 70
|||||||

DB 23 RRRARP 29

RESULT 12

O9T3Y9 PRELIMINARY; PRT: 245 AA.

AC O9T3Y9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 27.2 KDA PROTEIN.
OS Nephroselmis olivacea.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendreales; Chlorodendraceae; Nephroselmis.
OX NCBI_TaxId=31312;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-9938694; PubMed-10468594;
RX Tumei M., Otis C., Lemieux C.;
RA "The complete chloroplast DNA sequence of the green alga *Nephroselmis*
RT *olivacea*: Insights into the architecture of ancestral chloroplast
RT genomes."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC Tumei M., Otis C., Lemieux C.;
RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF137379; AAD54918.1; -
DR EMBL; AF137379; AAD54871.1; -
KW Hypothetical protein; Chloroplast.
SQ SEQUENCE 245 AA; 27217 MW; 74FDF5FD5F229FF7 CRC64;

Query Match 9.1%; Score 7; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSAL 24
|||||||

DB 204 TGLTSAL 210

RESULT 13

O92466 PRELIMINARY; PRT: 249 AA.

AC O92466;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACNMPV ORF106.
GN ORF.90.
OS Bombyx mori nuclear polyhedrosis virus (BmNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxId=10436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RX MEDLINE-97329351; PubMed-9185864;
RA Kamita S.G., Maeda S.;
*Sequencing of the putative DNA helicase-encoding gene of the Bombyx
RT mori nuclear polyhedrosis virus and fine-mapping of a region involved
RT in host range expansion."
RL Gene 190:173-178(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RX MEDLINE-99281911; PubMed-10355780;

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RA Genl S., Maizma K., Maeda S.;
RT *Sequence analysis of the genome of Bombyx mori
RT nucleopolyhedrovirus."
RL J. Gen. Virol. 80:1333-1337(1999).
RM (13)
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RA Maeda S.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RM (14)
RC SEQUENCE FROM N.A.
RC STRAIN-T3;
RA Genl S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: L33180; AAC63776.1; -
SO SEQUENCE 249 AA; 28921 MW; FC65F3EBBF298EF8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 12; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 ARPSLL 73
DB 194 ARPSLL 200

RESULT 14
O95WT5 PRELIMINARY; PRT; 309 AA.
ID 095WT5;
AC 095WT5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HOMEBOX HX.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OC NCBI_TaxID=7739;
OX (1)
RN SEQUENCE FROM N.A.
RP Kozmik Z., Vlcek C.;
RT "A novel homeobox gene in amphioxus."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF303216; AAL09323.1; -
SO SEQUENCE 309 AA; 34360 MW; B5ED048AF6E74FC CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 309;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 PPSLLQ 75
DB 262 PPSLLQ 268

RESULT 15
O9C9Z6 PRELIMINARY; PRT; 316 AA.
ID 09C9Z6;
AC 09C9Z6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOPHYSCAL 34.7 KDA PROTEIN (ATGCG8600/F17014_7).
GN F17014.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.

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RC STRAIN-CV, COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M.,
RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Oberaler B.,
RA Delseny M., Boutry M., Griuell L.A., Mache R., Puidomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brotlier P.,
RA Winkler P., Cactolico L., Weissenbach J., Saurin W., Queller F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Landie M., Berger-Liauro C., Purnelle B., Masny D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argitlou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Ruid S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Greasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
RA Pail G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Iodesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsuno M., Matsuno A., Mureki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Nakayama A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
RN (12)
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carinici P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamliya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN (13)
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carinici P., Dale J.M., Gibson H.A., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamliya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC012562; AAG51364.1; -
DR EMBL: AY056087; AAL06975.1; -
DR EMBL: AY045678; AAK74036.1; -
KW Hypothetical protein
SO SEQUENCE 316 AA; 34732 MW; SB54FCF59A5B5B CRC64;

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Query Match
Best Local Similarity 100.0%; Score 7; DB 10; Length 316;
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OY 22 SALNLP 28
DB 146 SALNLP 152

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Search completed: June 21, 2002, 08:24:58

job time: 283 sec
